

### REMARKS

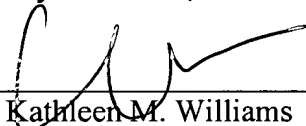
The Amendments directed herein are made in order to make the specification agree with the form of the Formal Figures submitted herewith. For clarity and in order to comply with U.S.P.T.O. rules regarding figures, the Formal Figures have been amended to change the scheme for indicating the location and identity of mutations in Figures 14 and 15.

In Figures 14 and 15, underlining of mutated residues in sequence printed on a regular white background is used instead of the dark shading of invariant residues and non-shading of mutated residues used in the figures as originally filed. Copies of the original Figures 14 and 15, plus clean and marked-up versions of amended Figures 14 and 15 are submitted herewith.

The amendments add no new matter. Entry of the amendments to the specification and Figures is respectfully requested. Entry of the Formal Figures as amended is also requested.

Date: 12/22/04

Respectfully submitted,



Name: Kathleen M. Williams  
Registration No.: 34,380  
Customer No.: 27495  
Palmer & Dodge LLP  
111 Huntington Avenue  
Boston, MA 02199-7613  
Tel. (617) 239-0100



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ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGC  
GAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATC  
GAAGAAATCAAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAG  
AAAAAGTTCTCGGCAGGTCTGTGGAGGTCTGGGTCTCTACTTTCACGCACCCGAGGACGTTCCGGCAATC  
CGCGACAAAATAAGGAAGCACCCCGCGGTTCATCGACATCTACGAGTACGACATACCTTCGCCAAGCGCTAC  
CTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAACTCATGTCTTCGACATCGAGACG  
CTCTACCACGAGGGAGAAGAGTTTGAACCGGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCG  
CGCGTGATAACCTGGAAGAAGATCGACCTTCCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAAG  
CGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGACGTGCTGATAACATAACGGCGACAACCTTCGACTTC  
GCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTTACCTCGGGAGGGACGGGAGCGAGCCGAAG  
ATACAGCCCATGGGGACAGGTTTTCGGTTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATA  
AGGGCGACCATAAACCTCCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAG  
AAGGTCTACGCCGAGGAGATAGCCACCGCTGCGGAGACCGCGAGGGGCTTGAGAGGGTCGCGCGCTACTCG  
ATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCCAGGCTC  
ATCGGCCAAGGCCTCTGGGACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGTTCTCTCTAAGGAAG  
GCCTACGAGAGGAACGAACTCGCTCCCAACAAGCCGACGAGAGGGAGCTGGCGAGGAGAAGGGGGGCTAC  
gcCGGTGGCTACGTCAAGGAGCCGGAGCGGGGACTGTGGGACAATATCGTGTATCTAGACTTTTCGTAGTCTC  
TACCTTCAATCATAATCACCCACAACGTCTCGCCAGATACGCTCAACCGCGAGGGGTGTAGGAGCTACGAC  
GTTGCCCCCGAGGTGGTCAAGTCTGCAAGGACTTCCCCGGCTTCATTCCGAGCCTGCTCGGAAACCTG  
CTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGAT  
TACAGGCAACGCGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATGCCAGGGCAAGATGG  
TACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGCTT  
GAGGAAAAGTTCGGTTTTAAAGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCTTGAGCGGAC  
GCTGAAACAGTCAAGAAAAGGCAATGGAGTTCTTAACTATATCAATCCCAAAGTCCCGGCTTCTCGAA  
CTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAGTACGCGGTTCATCGACGAGGAG  
GGCAAGATAACCACGCGCGGCTTGAGATAGTCAGGCGGACTGGAGCGAGATAGCGAAGGAGACGAGGCG  
AGGGTTTTGAGGGCGATACTCAGGCACGGTGACGTTGAAGAGGCGTCAGAATTGTCAGGGAAGTCACCGAA  
AAGCTGAGCAAGTACGAGGTTCCGCCGAGAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGAC  
TACAAGGCCACCGGCCGACGTAGCCATAGCGAAGcGTTTGGCCGCGAGAGGTGTTAAATCCGGCCCGGA  
ACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTC  
GACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATC  
CTCAGGGCTTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTGGGCTTGGCGCGTGG  
CTGAAGCCGAAGGGGAAGAAGAAGTGA

FIG. 1

MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDSALIEEIKKITAERHGRVVKVKRAEKVK  
KKFLGRSVEVWVLYFTHPQDVPARDKIRKHPAVIDIYDYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIET  
LYHEGEEFGTGPILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKEKDPDLITYNGDNFDF  
AYLKKRCEKLGVSFTLGRDGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKE  
KVYAEIATAWETGEGLERVARYSMEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTCNLVEWFLLRK  
AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYD  
VAPEVGHKFCKDFPGFIPSLGNNLEERQKIKRKMATLDPLEKNLLDYRQRAIKILANSYYGYGYARARW  
YCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLE  
LEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTE  
KLSKYEVPPEKLVIEHQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYIVLKGSGRIGDRAIPFDEF  
DPTKHKYDADYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

FIG. 2

MILDVDYITENGKPVIRVFKKENGFEFRIEYDREFEPYFYALLRDDSAIEE  
 IKKITAERHGRVVKVRAEKVKKKFLGRSVEVWVLYFTHPQDVP AIRDKI  
 RKHPAVIDIYEDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGE  
 EFGTGPILMISYADESEARVITWKKIDLPYEVVSTEKEMIKRFLRVVKE  
 KDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGRDGSEP KIQRMGDRFAV Extein 1  
 EVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEIATAWE  
 TEGGLERVARYSMEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTG  
 NLVEWFLLRKAYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNI  
 VYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFKCKDFPGFIP  
 SLLGNLLEERQKIKRKM KATLDPLEKNLLDYRQRAIKILAN

SLLPGEWVA  
 VIEGGLRPVRIGELVDGLMEASGERVKRDGDTEVLEVEGLYASPSTGSP  
 RKPAQCR\*KP\*\*GTAMPGKFTE\*LSTPEGGLSVTRGHS LFAYRDASLWR\*  
 RGRRRFKPGDLLAVPSG\*PSRRGGRGSTSLNCSSNCPRRKRPTCHRHSGK  
 GRKNFFRGMRLRTLWIFGEEKTGGRPGATWSTLRGLGYVKLRKIGYGVVD  
 REGLGKVPRFYERLVEVIRYNGNRGEFIADFNALRPVLR LMMPEKELEEW Intein 1  
 LVGTRNGFRIRPFIEVDWKFAKLLGYVSEGSAGKWK NRTGGWSYSVRLY  
 NEDGSVLDDMERLARSSLGA\*ARGELRRDFKEDGLHNLRGALRFTGREQE  
 GSVAYLHVP\*GGPLGLP\*GVLHRRRRRSPEQDGSALHQERASG\*RPRPAP  
 ELAGRLSDKRPPRQRLQGLRERG TALYRVPEAEERLTYSHVIPREVLEE  
 TSAGPSRRT\*VTGNSSGWWKAGSSTRKGPVG\*AGSSTGI\*SSTGSRKSGR  
 KATRGTSTT\*ALRRTRTSGGLWVPLRAQX

SYGYGYGYARARWYCRECAES  
 VTAWGREYIEMVIRELEEKFGFKVLYADTDGLHATIPGADAETVKKKAME  
 FLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVR  
 RDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEK LVI Extein 2  
 HEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYIVLKGSGRIGD  
 RAIPFDEFDPTKHKYDADYYIENQVLP AVERILRAFGYRKEDLRYQKTRQ  
 VGLGAWLKPKGKKK

FIG. 3

AATTCCACTGCCGTGTTTAACTTTCCACCGTTGAAC TTGAGGGTGATTT  
 TCTGAGCCTCCTCAATCACTTAATCGAGACCGCGATTACCTTGAAC TGG  
 TACACGTTCAACGATTCCGGTCTTGTAATGGTCGATACTGGGCCGTGCTG  
 GATTTTCTAAACGTCTCAAGAACGGCTTTCATCAACGGAACTGCCACGT 5' untranslated sequence  
 CTCCGCCGTGCTGAGGGTTAAACCTGAAGTTCAAGACTTTGCAACGGAAT  
 GGCAGAGAAACGGCGACTACCCAGTGGAAGAGCTTTTGAAAGCCAAAGC  
 CGAGCTTCAGCGAATGTGCGGTGCCCTTGTTCAAGAGTTGTGAGCCCTTG  
 ATTGTTGTTTTCTCCTCTTTTCTGATAACATCGATGGCGAAGTTTATTAG  
 TTCTCAGTTCGATAATCAGGCAGGTGTTGGTC

ATGATCCTTGACGTTGAT  
 TACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAA  
 CGGCGAGTT CAGGATTGAATACGACCGCGAGTT CGAGCCCTACTTCTACG  
 CGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCG  
 GAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAA  
 AAAGTTCTTCGGCAGGTCTGTGGAGGTCTGGGTCTCTACTTCACGCACC  
 CGCAGGACGTTCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGGTC  
 ATCGACATCTACGAGTACGACATACCCCTTCGCCAAGCGCTACCTCATAGA  
 CAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTCT  
 TCGACATCGAGACGCTCTACCACGAGGGAGAAGAGTTTGGAACCGGGCCG  
 ATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGCGTGATAACCTG  
 GAAGAAGATCGACCTTCCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGA  
 TGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTG  
 ATAACATAACAACGGCGACAACCTTCGACTTCGCCTACCTGAAAAAGCGCTG  
 TGAGAAGCTTGGCGTGAGCTTTACCCTCGGGAGGGACGGGAGCGAGCCGA Extein 1  
 AGATACAGCGCATGGGGACAGGTTTGCGGTGAGGTGAAGGCAGGGTA  
 CACTTCGACCTTTATCCAGTCATAAGGCGCACCATAAACCTCCCGACCTA  
 CACCCCTTGAGGCTGTATACGAGCGGTTTTTCGGCAAGCCCAAGGAGAAGG  
 TCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGGCTTGAG  
 AGGGTCGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGG  
 CAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAG  
 GCCTCTGGGACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTC  
 CTCTAAGGAAGGCCTACGAGAGGAACGAACTCGCTCCCAACAAGCCCGA  
 CGAGAGGGAGCTGGCGAGGAGAAGGGGGGGCTACGCCGGTGGCTACGTCA  
 AGGAGCCGGAGCGGGGACTGTGGGACAATATCGTGATCTAGACTTTTCGT  
 AGTCTCTACCCTTCAATCATAATCACCCACAACGTCTCGCCAGATACGCT  
 CAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCCGAGGTCGGTCACA  
 AGTTCTGCAAGGACTTCCCCGGCTTCATTCGAGCCTGCTCGGAAACCTG  
 CTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCC  
 GCTGGAGAAGAATCTCTCGATTACAGGCAACGCGCCATCAAGATTCTCG  
 CCAAC

FIG. 4

AGCCTTCTTCCCGGGAGTGGGTGCGGTCATTGAAGGGGGGAAA  
 CTCAGGCCCCGTCCGCATCGGCGAGCTGGTTGATGGACTGATGGAAGCCAG  
 CGGGGAGAGGGTGAAAAGAGACGGCGACACCGAGGTCTTGAAGTCGAGG  
 GGCTTTACGCTCTCCTTCGACAGGGAGTCCAAGAAAGCCCGCACAAATGC  
 CGGTGAAAGCCGTGATAAGGCACCGCTATGCCGGGGAAGTTTACAGAATA  
 GCTCTCAACTCCGGAAGGAGGATTAAGCGTGACGCGCGCCACAGCCTCT  
 TCGCGTACCGGGACGCGAGCTTGTGGAGGTGACGGGGGAGGAGGAGTTC  
 AAGCCCGGCGACCTCCTGGCGGTGCCAAGCGGATAACCCCTCCCGGAGAGG  
 AGGGAGAGGCTCAACATCGTTGAACTGCTCCTCGAACTGCCCGAGGAGGA  
 AACGGCCGACATGTCATCGACATTCCGGCAAGGGTAGAAAGAACTTCTTC  
 AGGGGAATGCTCAGAACCCTCCGCTGGATTTTCGGGGAGGAGAAGACCCG Intein 1  
 AGGGCGGCCAGGCGCTACCTGGAGCACCTTGCGTGGGCTCGGCTACGTGA  
 AGCTGAGGAAAATCGGCTACGGGGTGGTTGATAGGGAGGGAAGTGGGAAA  
 GTACCGCGCTTCTACGAGAGGCTCGTGGAGGTAATCCGCTACAACGGCAA  
 CAGGGGGGAGTTCATCGCCGATTTCAACGCGCTCCGCCCCGTCTCCGCC  
 TGATGATGCCCGAGAAGGAGCTTGAAGAGTGGCTCGTTGGGACGAGGAAC  
 GGGTTTCAGGATAAGGCGGTTTCATAGAGGTTGATTGGAAGTTCGCAAAGCT  
 CCTCGGCTACTACGTGAGCGAGGGGAGCGCCGGGAAGTGGAAAAACCGGA  
 CCGGGGGCTGGAGCTACTCGGTGAGGCTTTACAACGAGGACGGGAGCGTT  
 CTCGACGACATGGAGAGACTCGCGAGGAGTTCTTTGGGGGCGTGAGCGCG  
 GGGGGAACACGTCGAGATTTCAAAGAAGATGGCCTACATAATCTTCGAG  
 GGGCTCTGCGGTTACCGGCCGAGAACAAGAGGGTTCCGTGGCTTATCTT  
 CACGTCCCCTGAGGAGGTCCGCTGGGCCTTCCTTGAGGGGTACTTCATCG  
 GCGACGGCGACGTTACCCGAGCAAGATGGTTCCGGCTCTCCACCAAGAGC  
 GAGCTTCTGGCTAACGGCCTCGTCCTGCTCCTGAACTCGCTGGGCGTCTC  
 AGCGATAAACGTCCGCCACGACAGCGGGGTTTACAGGGTCTACGTGAACG  
 AGGAACTGCCCTTTACAGAGTACCGGAAGCGGAAGAACCCTCACTTACT  
 CCCACGTCATACCGAGGGAAGTGCTGGAGGAGACTTCGGCCGGGCTTCC  
 AGAAGAACATGAGTCACGGGAAATTACGGGAGCTGGTGGAAAGCGGGGAG  
 CTCGACGCGGAAGGGCCGGTAGGATAGGCTGGCTCCTCGACGGGGATAT  
 AGTCCTCGACAGGGTCTCGGAAGTCAGGAAGGAAAGCTACGAGGGGTACG  
 TCTACGACCTGAGCGTTGAGGAGGACGAGAACTTCTGGCGGGCTTTGGGT  
 TCCTCTACGCGCACAAACNN

FIG. 4 (cont.)

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AGCTACTACGGCTACTACGGCTATGCCAGGG  
CAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGG  
GAGTACATCGAAATGGTCATCAGAGAGCTTGAGGAAAAGTTCGGTTTTAA  
AGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCTGGAGCGG  
ACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAAT  
CCCAAAGTGGCCGGCCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAG  
GGGCTTCTTCGTACGAAGAAAAAGTACGCGGTATCGACGAGGAGGGCA  
AGATAACCACGCGCGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATA  
GCGAAGGAGACGCAGGCGAGGGTTTTGGAGGCGATACTCAGGCACGGTGA Extein 2  
CGTTGAAGAGGCCGTCAGAATTGTCAGGGAAGTCACCGAAAAGCTGAGCA  
AGTACGAGGTTCCGCCGAGAAGCTGGTTATCCACGAGCAGATAACGCGC  
GAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAGCG  
TTTGCGCCGAGAGGTGTTAAATCCGGCCCGGAACGTGATAAGCTACA  
TCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGAC

GAGTTCGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAA  
CCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCA  
AGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGCGCGTGG  
CTGAAGCCGAAGGGGAAGAAGAAGTGA

GGAATTATCTGGTTTCTTTTCCC  
AGCATTAAATGCTTCCGACATTGCCTTATTTATGAACTCCTGTGTGCC  
TGAGTTTGTGCCAGAAAACAGCCTGTTCTGACGGCGCTTTTCTTGCCAG  
GTCCTTTGAGTTTCGCAAGGGTCTTCTCGACCAGCTCAATGGTCTTGTCG  
TCATTGTTTNNNNNNNNNNNNNNNNNNNNCCCGGGACTTCATACTGGC  
GGTAATAGACAGGGATTCTTCTCAAGGACTTCCCGGGAGGCATTGGAG  
TTTTTTGGTGGGGCTTTCACAGGATTGCTCATCTTGTGGATTCTCGTT  
CGATTGAATCTGTCCACTTGAGGGTGTAGGTCGAGACGGTGGAGCGCGTA  
TTCCGGGAGCGGGTCTTGAGGCTCCATTTTTAGTCTCCTCCGGCGAAG 3' Untranslated sequence  
AAGTGGAATCAAGCCGGGTGTTAGCTTATGTTATGTTCCCAACTCCTCC  
AGCACCTCCAGGATCCCCCAATCCCGGAACCTCGAAGCCCCCTCTCGTGG  
ATCTTTCTAACTTCTCTGCCTCCGGGTTTATCCAGACCGCCACATGCC  
GGCTCTCAGCGACCCCTCGAAATCCTCCGCGTAGGTGTCGCGGATGTGGA  
TTGCCCTCGTCCGGCTCGACCCCGAAGCATCGAGCGGTTTTCTGAACATCT  
CGGGCATCGGCTTATACGCCAGAACCTCGTCGGCGAAGAAGGTTCCCTCA  
ATGTAGTCCATCAGGCCGAACCTCTCGAGGGGGGGCCCGGTACCCAATTC  
GCCCTATAGTGAGTCGATTACAATTCAGTGGCCGTCGTTTTACAACGTCG  
TGACTGGGAAAACCTGGCGTTACCCAACCTAAGTCGCTTTCAGCACAT  
CCCCC

FIG. 4 (cont.)

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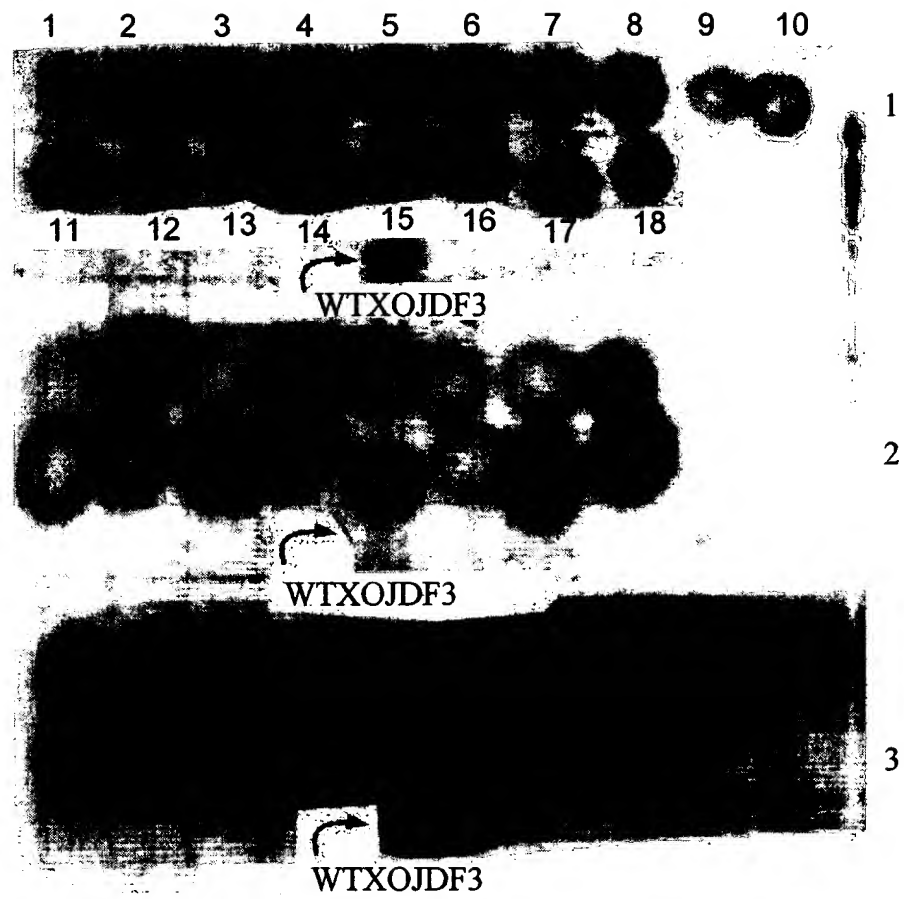


FIG. 5



Sequencing with Purified Mutants



FIG. 6

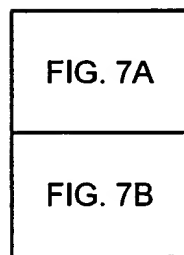
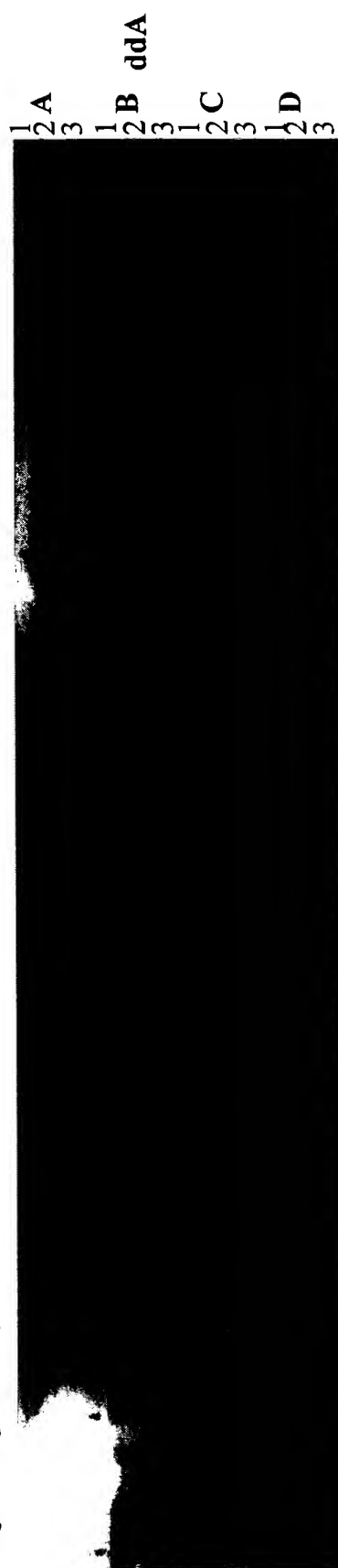


FIG. 7

Sequencing with Dye-labeled Dideoxynucleotides



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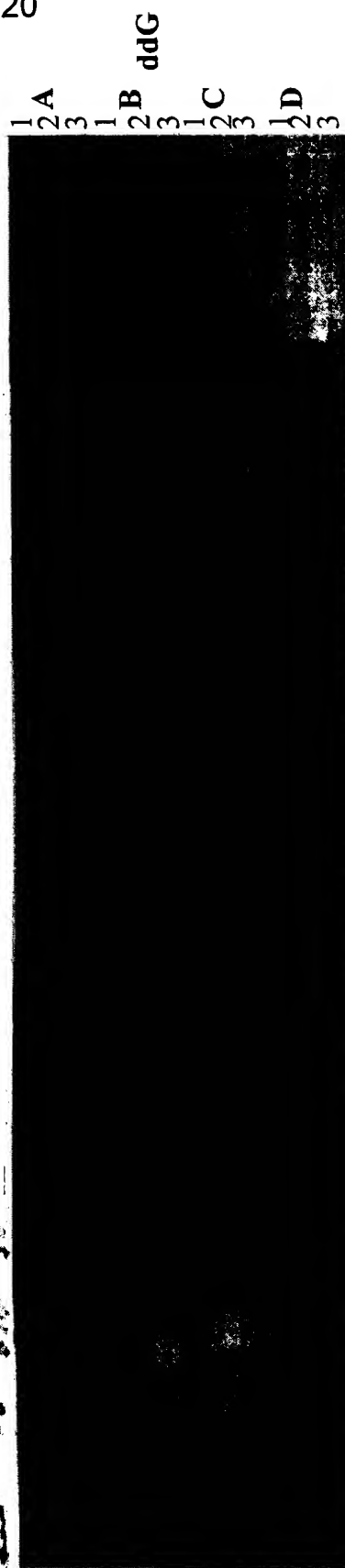


FIG. 7A

1A  
2A  
3A  
1B  
2B  
3B  
1C  
2C  
3C  
1D  
2D  
3D

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ddC

1A  
2A  
3A  
1B  
2B  
3B  
1C  
2C  
3C  
1D  
2D  
3D

ddT

FIG. 7B

Sequencing with the P410L, A485T Double Mutant and  $\alpha$ - $^{33}$ P Dideoxynucleotides



FIG. 8

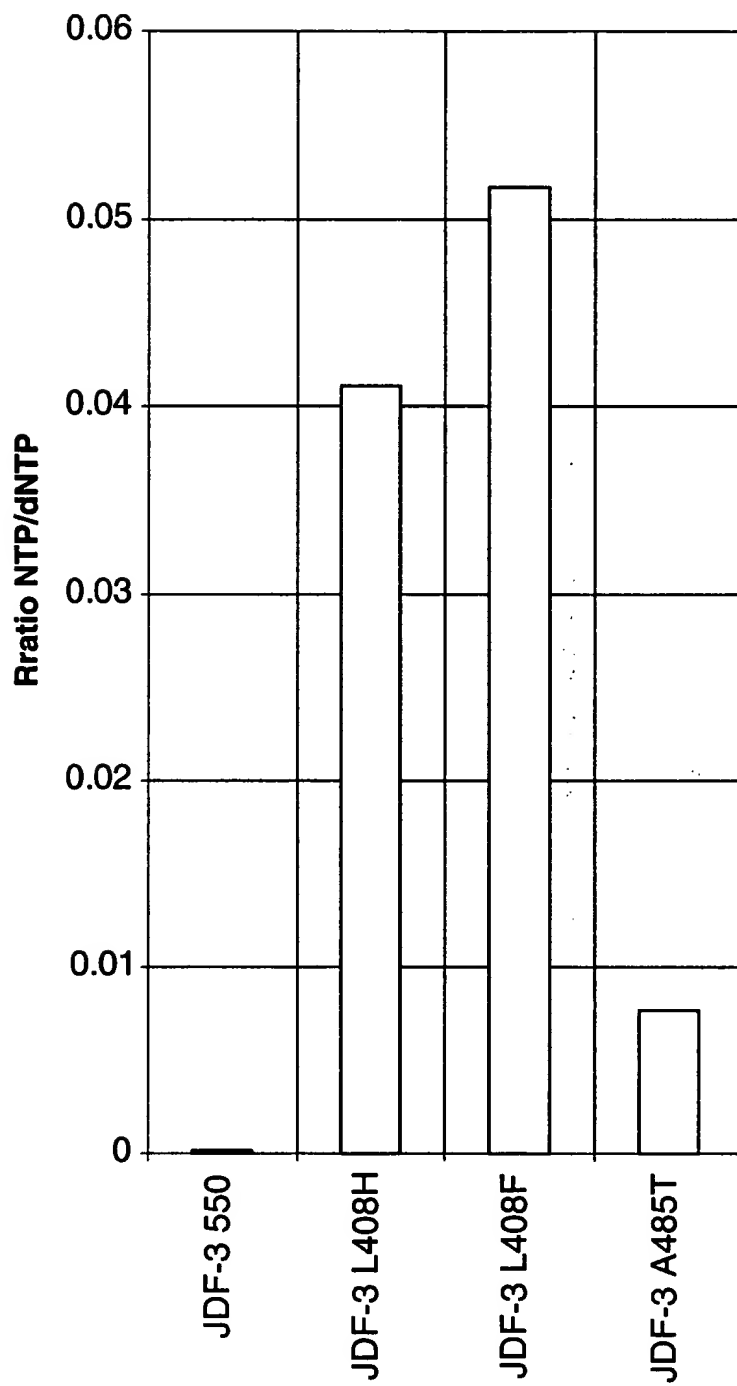


FIG. 9

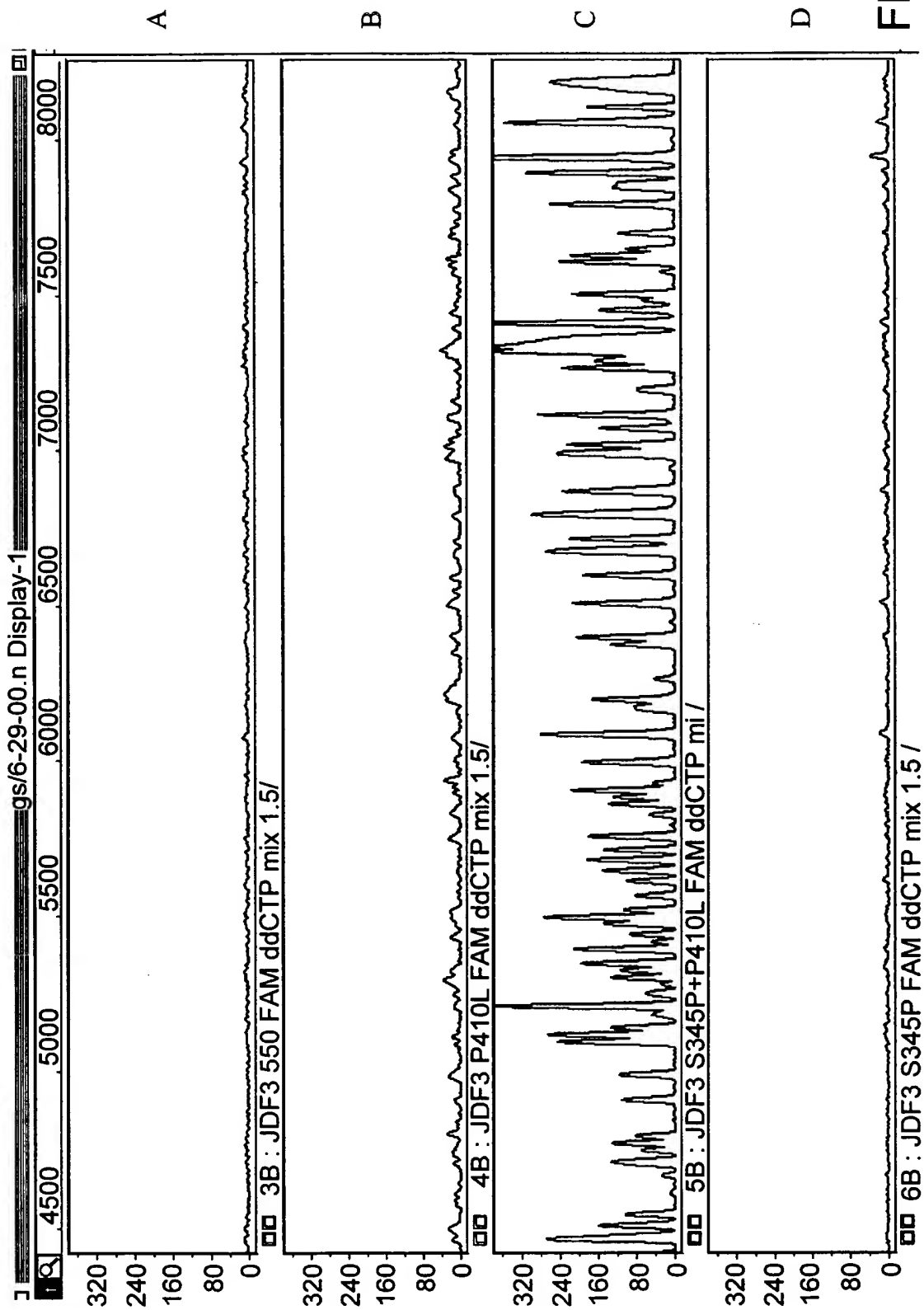


FIG. 10

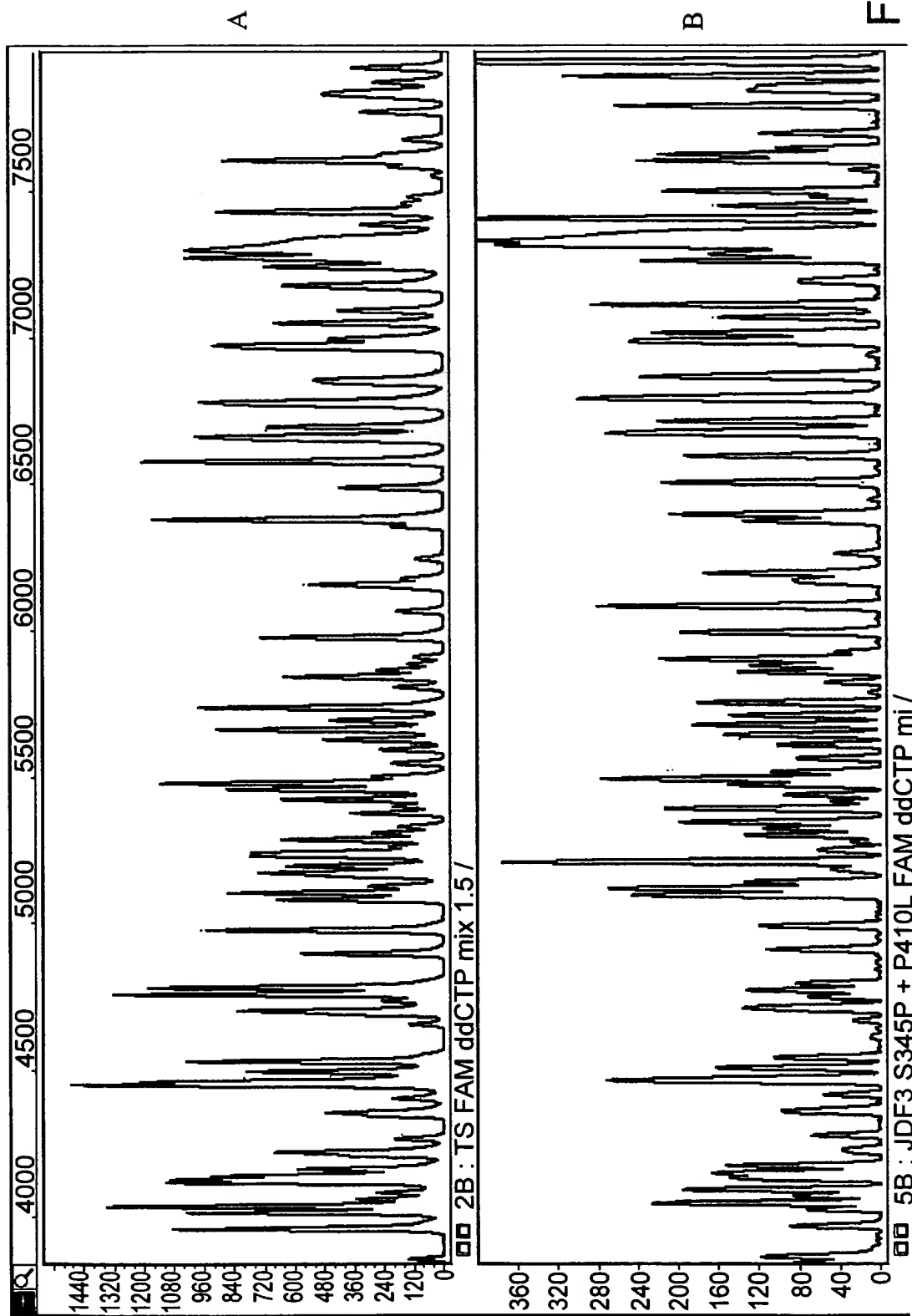


FIG. 11

**<sup>33</sup>P**-TAACGTTGGGGGGGCA →  
 TGAACCCCCCCCCGTAT

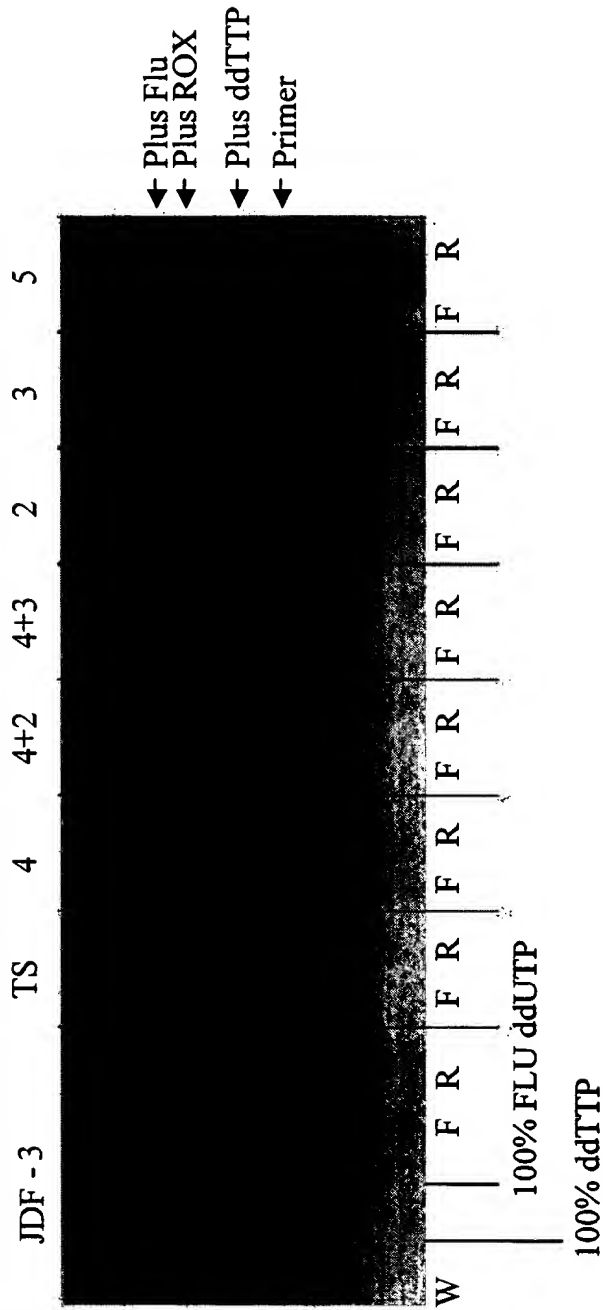
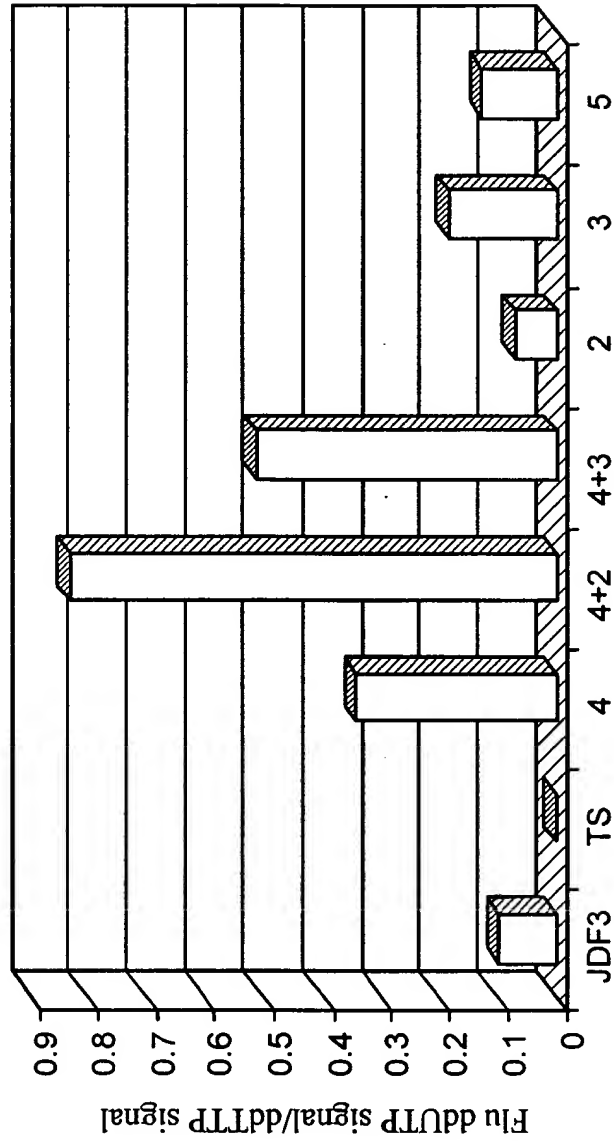


FIG. 12





Mutants

FIG. 13

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*Shading  
removed. Mutations  
indicated by  
under lining*

4 1 -----LVXNAXSTGNLVEWFLLRK  
10 1 -----VWDVSRSTGNLVERFLLRK  
13 1 -----VWDVSRSTGNLVEWFLLRK  
16 1 -----VWDVSRSTGNLVEWFLLRK  
18 1 -----VWDVSRSTGNLVEWFLLRK  
19 1 -----VWDVSRSTGNLVEWFLLRK  
28 1 -----VWDVPRSTGNLVEWFLLRK  
34 1 -----VWDVSRSTGNLVEWFLLRK  
41 1 -----VWDVSRSTGNLVEWFLLRK  
33 1 -----VWDVSRSTGNLVEWFLLRK  
48 1 -----YWSXPXLRTGNLVEWFLLRK  
55 1 -----VLGTXPSTGNLVEWFLLRK  
64 1 -----XXXFWDVSRSTGNLVEWFLLRK

Jdf3 301 TGEGLERVARYSMEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRK  
310 320 330 340 350 360

4 20 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP  
10 21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHSVSP  
13 21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP  
16 21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP  
18 21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP  
19 21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGQWDNIA\_YLDFRSLYPSIIITHNVSP  
28 21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP  
34 21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP  
41 21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGPWDNIVYLDFRSLYPSIIITHNVSP  
33 21 AYERNKLAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP  
48 21 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP  
55 22 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSHYPSIIITHNVSP  
64 24 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP

Jdf3 361 AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP  
370 380 390 400 410 420

FIG. 14

Shading Removed -  
Mutation indicated by  
underlining

4 80 DTLNREGCRSYDVAPEVGHKFKDFPGFI PSL LGN LLEERQKIKRKM KATLDPLEKNLLD  
10 81 DTLNREGCRSYDVAPEVGHKFKDFPGFI PSL LGN LLEERQKIKRKM KATLDPLEKNLLD  
13 81 DTLNREGCRSYDVAPEVGHKFKDFPGFI PSL LGN LLEERQKIKRKM KATLDPLEKNLLD  
16 81 DTLNREGCRSYDVAPEVGHKFKDFPGFI PSL LGN LLEERQKIKRKM KATLDPLEKNLLD  
18 81 DTLNREGCRSYDVAPEVGHKFKDFPGFI PSL LGN LLEERQKIKRKM KATLDPLEKNLLD  
19 81 DTLNREGCRSYDVAPEVGHKFKDFPGFI PSL LGN LLEERQKIKRKM KATLDPLEKNLLD  
28 81 DTLNREGCRSYDVAPEVGHKFKDFPGFI PSL LGN LLEERQKIKRKM KATLDPLEKNLLD  
34 81 DTLNREGCRSYDVAPEVGHKFKDFPGFI PSL LGN LLEERQKIKRKM KATLDPLEKNLLD  
41 81 DTLNREGCRSYDVAPEVGHKFKDFPGFI PSL LGN LLEERQKIKRKM KATLDPLEKNLLD  
33 81 DTLNREGCRSYDVAPEVGHKFKDFPGFI PSL LGN LLEERQKIKRKM KATLDPLEKNLLD  
48 81 DTLNREGCRSYDVAPEVGHKFKDFPGFI PSL LGN LLEERQKIKRKM KATLDPLEKNLLD  
55 82 DTLNREGCRSYDVAPEDGHKFKDFPGFI PSL LGN LLEERQKIKRKM KATLDPLEKNHLLD  
64 84 DTLNREGCRSYDVAPEVGHKFKDFPGFI PSL LGN LLEERQKIKRKM KATLDPLEKNLLD  
Jdf3 421 DTLNREGCRSYDVAPEVGHKFKDFPGFI PSL LGN LLEERQKIKRKM KATLDPLEKNLLD  
430 440 450 460 470 480

FIG. 14 (cont.)

Shading  
removed - Mutations  
indicated by  
underlining

4 140 YRQRAIKILANSYYGYCGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
10 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
13 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
16 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
18 141 YRQRAIKILANYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
19 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
28 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
34 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
41 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
33 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
48 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
55 142 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
64 144 YRQRAIKILANSYYGNYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
Jdf3 481 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD

490 500

4 200 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
10 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
13 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
16 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELKYEGFYVRGFFVTKKKYAVIDEE  
18 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
19 201 TDGLHATIPGADAETVKKKAMEFLNYINLKLPGLELEYEGFYVRGFFVTKKKXAVIDEE  
28 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
34 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
41 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
33 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLEPEYEGFYVRGFFVTKKKYAVIDEE  
48 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
55 202 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
64 204 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
Jdf3 541 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE

550 560 570 580 590 600

FIG. 15

Shading removed -  
Mutations indicated  
by underlining

4 260 GKITTRGLEIVRRDWSEIAKETQARVLEAVLRHGDVEEAVRIVREVTEKLSKYEVPPEKL  
10 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEEL  
13 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVRKVTEKLSKYEVPPEKL  
16 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKL  
18 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHDDVEEAVRIVREVTEKLSKYEVPPEKL  
19 261 GKITTRGLEIVRRDWSKIAKETQARVLEAILRHGDVEEAI RIVREVTEKLSKYEVPPEKL  
28 261 GKIA TRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKL  
34 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLNKYEVPPEKL  
41 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKL  
33 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKL  
48 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPVKL  
55 262 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVP PGEA  
64 264 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKL  
Jdf3 601 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKL  
610 620 630 640 650 660

FIG. 15 (cont.)